

## RESULT 5

A26054

asparaginase (EC 3.5.1.1) precursor - *Erwinia chrysanthemi*C;Species: *Erwinia chrysanthemi*

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 31-Dec-2004

C;Accession: A26054; S03681

R;Minton, N.P.; Bullman, H.M.S.; Scawen, M.D.; Atkinson, T.; Gilbert, H.J.

Gene 46, 25-35, 1986

A;Title: Nucleotide sequence of the *Erwinia chrysanthemi* NCPPB 1066 L-asparaginase gene.

A;Reference number: A26054; MUID:87106840; PMID:3026924

A;Accession: A26054

A;Molecule type: DNA

A;Residues: 1-348 &lt;MIN&gt;

A;Cross-references: UNIPROT:P06608; UNIPARC:UPI000002C8D8; GB:M14741; GB:X14777;

NID:g42965; PIDN:CAA32884.1; PID:g4185897

A;Note: the authors translated the codon AAG for residue 286 as Leu

R;Filpula, D.; Nagle, J.W.; Pulford, S.; Anderson, D.M.

Nucleic Acids Res. 16, 10385, 1988

A;Title: Sequence of L-asparaginase gene from *Erwinia chrysanthemi* NCPPB 1125.

A;Reference number: S03681; MUID:89057497; PMID:3194219

A;Accession: S03681

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-176,'I',178-198,'R',200-287,'L',289-294,'M',296-348 &lt;FIL&gt;

A;Cross-references: UNIPARC:UPI000016EE0D; GB:X12746; NID:g40993; PIDN:CAA31239.1;

PID:g40994

C;Superfamily: L-asparaginase/Glutamyl-tRNA(Gln) amidotransferase subunit D

C;Keywords: hydrolase

F;1-21/Domain: signal sequence #status predicted &lt;SIG&gt;

F;22-348/Product: asparaginase #status predicted &lt;MAT&gt;

Query Match 38.0%; Score 716; DB 1; Length 348;

Best Local Similarity 46.7%; Pred. No. 1.9e-40;

Matches 163; Conservative 59; Mismatches 103; Indels 24; Gaps 8;

Qy 30 FVFTNANGLNFTQMNTTLPNVTFATGGTIAGSDSSSTATTTGYTSGAVGVLSLIDAVPSM 89

Db 15 FVFT-----ASAADKLPNIVILATGGTIAGSAATGTQTTGYKAGALGVDTLINAVPEV 67

Qy 90 LDVANVAGVQVANVGSEDTSDILISMSKKLNRVVCEDPTMAGAVITHGTDLTLEETAFFL 149

Db 68 KKLANVKGEQFSNMASENMTGDVVCLKSQRVNELLARD-DVDGVVITHGTDLTVEESAYFL 126

Qy 150 DATVNCCKPIVIVGAMRPSTAISADGPFNLLEAVTVAASTSARDRGAMVVMNDRIASAYY 209

Db 127 HLTVKSDKPVVFAAMRPATAISADGPMNLLEAVRVAGDKQSRGRGVMVVLNDRIGSARY 186

Qy 210 VTKTNANTMDTFKAMEMGYLGEMISNTPFFFPVK-PTGKVAFDITNVTEIPRVDILFS 268

Db 187 ITKTNASTLDTFKANEELGYLGVIIIGNRIYYQNRIDKLHTTRSVFDVRGLTSLPKVDILYG 246

Qy 269 YEDMHNHTLYN-AISSGAQGIVIAAGAGGVT---TSFNEAIEDVINRLEIPVQSMRT 323

Db 247 YQD-DPEYLYDAAIQHGVKGIVYAGMGAGSVSVRGIAGMRKAMEK-----GVVIRSTR 300

Qy 324 VNGEVPLSDVSSDTATHIASGYLNPQKSRILLGILLSQGKNITEIADV 372

Db 301 GNGIVP----PDEELPGLVSDSLNPAHARILLMLALTRTSDPKVIQYEF 345